



# An Information Portal to Biological Macromolecular Structures

As of Tuesday Feb 28, 2006 there are 35343 Structures | PDB Statistics

☒ PDB ID or keyword ☐ Author   ☐ Advanced Search

Home Search Results Queries

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Match all of the following conditions:


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Between: 83.92 and 93.68	
a (angstroms)	
Between: 83.92 and 93.68	
b (angstroms)	
Between: 166.24 and 183.74	
c (angstroms)	
Between: 90 and 90	
alpha (degrees)	
Between: 90 and 90	
beta (degrees)	
Between: 90 and 90	
gamma (degrees)	

Materials & Methods  
X-Ray Cell Dimensions

☒ 13 Structures

Choose a Query Type:

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☐ Remove Similar Sequences at 90% Identity

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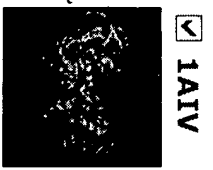
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P4322



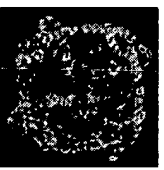
**1AIV**

**Characteristics**  
**Classification**  
**Compound**  
**Authors**

**APO OVOTRANSFERRIN**

Release Date: 29-Apr-1998 Exp. Method: X Ray Diffraction  
Resolution: 3.00 Å  
**Iron Transport Protein**  
Mol. Id: 1 Molecule: Ovotransferrin  
Kurokawa, H., Dewan, J.C., Mikami, B., Sacchettini, J.C., Hirose, M.

I422



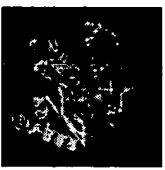
**1J4N**

**Characteristics**  
**Classification**  
**Compound**  
**Authors**

**Crystal Structure of the AQP1 water channel**

Release Date: 27-Mar-2002 Exp. Method: X Ray Diffraction  
Resolution: 2.20 Å  
**Membrane Protein**  
Mol. Id: 1 Molecule: Aquaporin 1  
Sui, H., Han, B.G., Lee, J.K., Walian, P., Jap, B.K.

I422



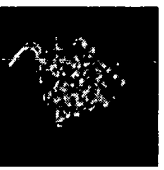
**1KYH**

**Characteristics**  
**Classification**  
**Compound**  
**Authors**

**Structural Genomics, Hypothetical protein in SIGY-CYDD intergenic region**

Release Date: 14-Aug-2002 Exp. Method: X Ray Diffraction  
Resolution: 1.60 Å  
**Structural Genomics Unknown Function**  
Mol. Id: 1 Molecule: Hypothetical 29.9 Kda Protein in Sigy Cydd Intergenic Region  
Zhang, R.G., Grembecka, J., Vinokour, E., Collart, F., Dementieva, I., Minor, W., Joachimiak, A.

P212121



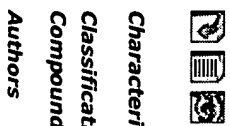
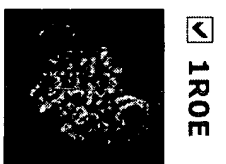
**1Q4L**

**Characteristics**  
**Classification**  
**Compound**  
**Authors**

**GSK-3 Beta complexed with Inhibitor I-5**

Release Date: 14-Oct-2003 Exp. Method: X Ray Diffraction  
Resolution: 2.77 Å  
**Transferase**  
Mol. Id: 1 Molecule: Glycogen Synthase Kinase 3 Beta  
Bertrand, J.A., Thierffine, S., Vulpetti, A., Cristiani, C., Valsasina, B., Knapp, S., Kalisz, H.M., Flocco, M.

P212121

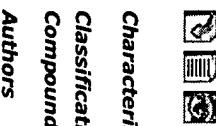
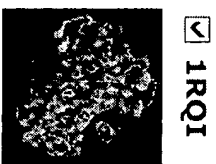


Characteristics  
Classification  
Compound  
Authors

Glycogen synthase kinase-3 beta in complex with 3-indolyl-4-arylmaleimide inhibitor  
Release Date: 12-Oct-2004 Exp. Method: X Ray Diffraction  
Resolution: 2.25 Å  
Transferase  
Mol. Id: 1 Molecule: Glycogen Synthase Kinase 3 Beta  
Allard, J., Nikolcheva, T., Gong, L., Wang, J., Dunten, P., Avnur, Z., Waters, R., Sun, Q., Skinner, B.

P4122

Not disclosed by  
instant  
applicants + →

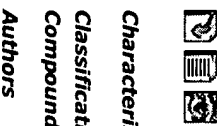


Characteristics  
Classification  
Compound  
Authors

Active Conformation of Farnesyl Pyrophosphate Synthase Bound to Isopentyl Pyrophosphate and Dimethylallyl S-Thiolodiphosphate  
Release Date: 02-Mar-2004 Exp. Method: X Ray Diffraction  
Resolution: 2.42 Å  
Transferase  
Mol. Id: 1 Molecule: Geranyltransferase  
Hosfield, D.J., Zhang, Y., Dougan, D.R., Brooun, A., Tari, L.W., Swanson, R.V., Finn, J.

P4122

The instant  
application ⇒



Characteristics  
Classification  
Compound  
Authors

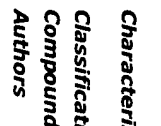
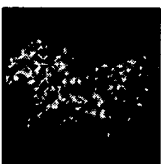
Active Conformation of Farnesyl Pyrophosphate Synthase Bound to Isopentyl Pyrophosphate and Risedronate  
Release Date: 02-Mar-2004 Exp. Method: X Ray Diffraction  
Resolution: 1.95 Å  
Transferase  
Mol. Id: 1 Molecule: Geranyltransferase  
Hosfield, D.J., Zhang, Y., Dougan, D.R., Brooun, A., Tari, L.W., Swanson, R.V., Finn, J.



Characteristics  
Classification  
Compound  
Authors

Crystal structure of hen serum transferrin in apo-form

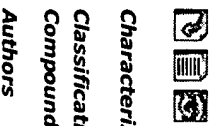
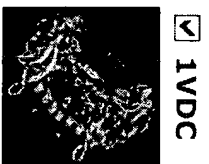
P43212



Characteristics  
Classification  
Compound  
Authors

Release Date: 13-Jul-2004 Exp. Method: X Ray Diffraction  
Resolution: 3.50 Å  
Metal Transport  
Mol. Id: 1 Molecule: Ovotransferrin  
Thakurta, P.G., Choudhury, D., Dasgupta, R., Dattagupta, J.K.

P41212



Characteristics  
Classification  
Compound  
Authors

STRUCTURE OF NADPH DEPENDENT THIOREDOXIN REDUCTASE  
Release Date: 12-Mar-1997 Exp. Method: X Ray Diffraction  
Resolution: 2.50 Å  
Oxidoreductase  
Mol. Id: 1 Molecule: NADPH Dependent Thioredoxin Reductase  
Dai, S., Saarinen, M., Ramaswamy, S., Meyer, Y., Jacquot, J.P., Eklund, H.

p4322

☒ 1YKH

## Structure of the mediator MED7/MED21 (Med7/Srb7) subcomplex

## Characteristics

Release Date: 22-Feb-2005 Exp. Method: X Ray Diffraction  
Resolution: 3.00 Å

## Classification

## Gene Regulation

Mol. Id: 1 Molecule: RNA Polymerase II Mediator Complex Protein Med7

Fragment: Residues 102-205 Mol. Id: 2 Molecule: RNA Polymerase II Holoenzyme

Component Srb7 Mutation: LSM, L119M, L125M

## Compound

## Authors

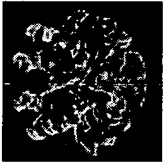

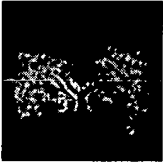
Baumli, S., Hoepfner, S., Cramer, P.



1 2 ⇌

Home Search Results Queries

1 2

<input checked="" type="checkbox"/> Results (11-13 of 13) <input checked="" type="checkbox"/> Refine this Search <input checked="" type="checkbox"/> Select All <input checked="" type="checkbox"/> Deselect All <input checked="" type="checkbox"/> Download Selected <input type="checkbox"/> Tabulate <input type="checkbox"/> Narrow Query <input type="checkbox"/> Sort Results <input type="checkbox"/> Results per Page <input checked="" type="checkbox"/> Show Query Details <input type="button" value="Results Help"/>	 <p><b>1ZP6</b></p> <p><b>Characteristics</b>  <b>Classification</b>  <b>Compound</b>  <b>Authors</b></p> <p>Crystal Structure of Atu3015, a Putative Cytidylate Kinase from Agrobacterium tumefaciens, Northeast Structural Genomics Target Atr62            Release Date: 24-May-2005 Exp. Method: X Ray Diffraction            Resolution: 3.20 Å  <b>Structural Genomics Unknown Function</b>            Mol. Id: 1 Molecule: Hypothetical Protein Atu3015            Forouhar, F., Abashidze, M., Vorobiev, S.M., Kuzin, A., Conover, K., Acton, T.B., Montelione, G.T., Hunt, J.F., Tong, L.</p>
 <p><b>2AYU</b></p> <p><b>Characteristics</b>  <b>Classification</b>  <b>Compound</b>  <b>Authors</b></p> <p>The structure of nucleosome assembly protein suggests a mechanism for histone binding and shuttling            Release Date: 07-Feb-2006 Exp. Method: X Ray Diffraction            Resolution: 3.00 Å  <b>Chaperone</b>            Mol. Id: 1 Molecule: Nucleosome Assembly Protein            Park, Y.J., Luger, K.</p>	 <p><b>2BAS</b></p> <p><b>Characteristics</b>  <b>Classification</b>  <b>Compound</b>  <b>Authors</b></p> <p>Crystal structure of a complex between PTP1B and the insulin receptor tyrosine kinase            Release Date: 15-Nov-2005 Exp. Method: X Ray Diffraction            Resolution: 2.30 Å  <b>Hydrolase/transferase</b>            Mol. Id: 1 Molecule: Tyrosine Protein Phosphatase Non Receptor Type 1 Mol. Id: 2            Molecule: Insulin Receptor Fragment: Protein Kinase            Li, S., Depetris, R.S., Barford, D., Chernoff, J., Hubbard, S.R.</p>

1 2

STN search  
10/651668

(unit cell dimensions)

=> d his

(FILE 'HOME' ENTERED AT 16:25:07 ON 01 MAR 2006)

FILE 'CAPLUS' ENTERED AT 16:25:39 ON 01 MAR 2006

L1 1840516 S PROTEIN  
L2 1805951 S ?CRYSTAL?  
L3 52256 S L1 AND L2  
L4 649 S L3 AND (UNIT CELL DIMENSION#)  
L5 25 S L4 AND 88  
L6 2 S L5 AND 174  
L7 ~~26 S L3 AND 14122~~  
L8 ~~666 S L3 AND TETRAGONAL~~  
L9 ~~26 S L7 AND L3~~  
L10 ~~0 S L6 AND L8~~

=> d L6 1-2

L6 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2006 ACS on STN

AN 1998:463974 CAPLUS

DN 129:199494

TI An internal affinity-tag for purification and crystallization of  
the siderophore receptor FhuA, integral outer membrane protein  
from Escherichia coli K-12

AU Ferguson, Andrew D.; Breed, Jason; Diederichs, Kay; Welte, Wolfram;  
Coulton, James W.

CS Department of Microbiology and Immunology, McGill University, Montreal,  
QC, H3A 2B4, Can. →

SO Protein Science (1998), 7(7), 1636-1638 Mar, 6, 998

CODEN: PRCIEI; ISSN: 0961-8368

PB Cambridge University Press

DT Journal

LA English

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

unit cell dimension of  
 $a = b = 174 \text{ \AA}$   
 $c = 88 \text{ \AA}$   
 $\alpha = \beta = 90^\circ, \gamma = 120^\circ$

L6 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2006 ACS on STN

AN 1998:224997 CAPLUS

DN 128:318765

TI Crystallization of NAD<sup>+</sup>-dependent phenylalanine dehydrogenase  
from Nocardia sp239

AU Pasquo, A.; Britton, K. L.; Baker, P. J.; Brearley, G.; Hinton, R. J.;  
Moir, A. J. G.; Stillman, T. J.; Rice, D. W.

CS Krebs Institute for Biomolecular Research, Department of Molecular Biology  
and Biotechnology, University of Sheffield, Sheffield, S10 2TN, UK →

SO Acta Crystallographica, Section D: Biological Crystallography (1998),  
D54(2), 269-272 Mar 1

CODEN: ABCRE6; ISSN: 0907-4449

PB Munksgaard International Publishers Ltd.

DT Journal

LA English

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

$a = b = 111.0 \text{ \AA}$   
 $c = 174.5 \text{ \AA}$   
 $\alpha = \beta = 90^\circ$   
 $\gamma = 120^\circ$